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(54) Parallel information display system.

(57) A parallel information display system includes a display (6), a memory (4) for storing at least a sequence name and elements of a sequence for a plurality of sequences, a keyboard (7) having keys for specifying a plurality of sequences to be displayed on the display, and a controller (8) for controlling at least a read operation from the memory (4) responsive to the manipulation of the keys so that the sequence names and the elements of the specified sequences are displayed on the display (6) in units of blocks. Each of the blocks include the elements of the specified sequences displayed in adjacent lines in correspondence with the sequence names. Each line is made up of a predetermined number of the elements of one of the specified sequences.

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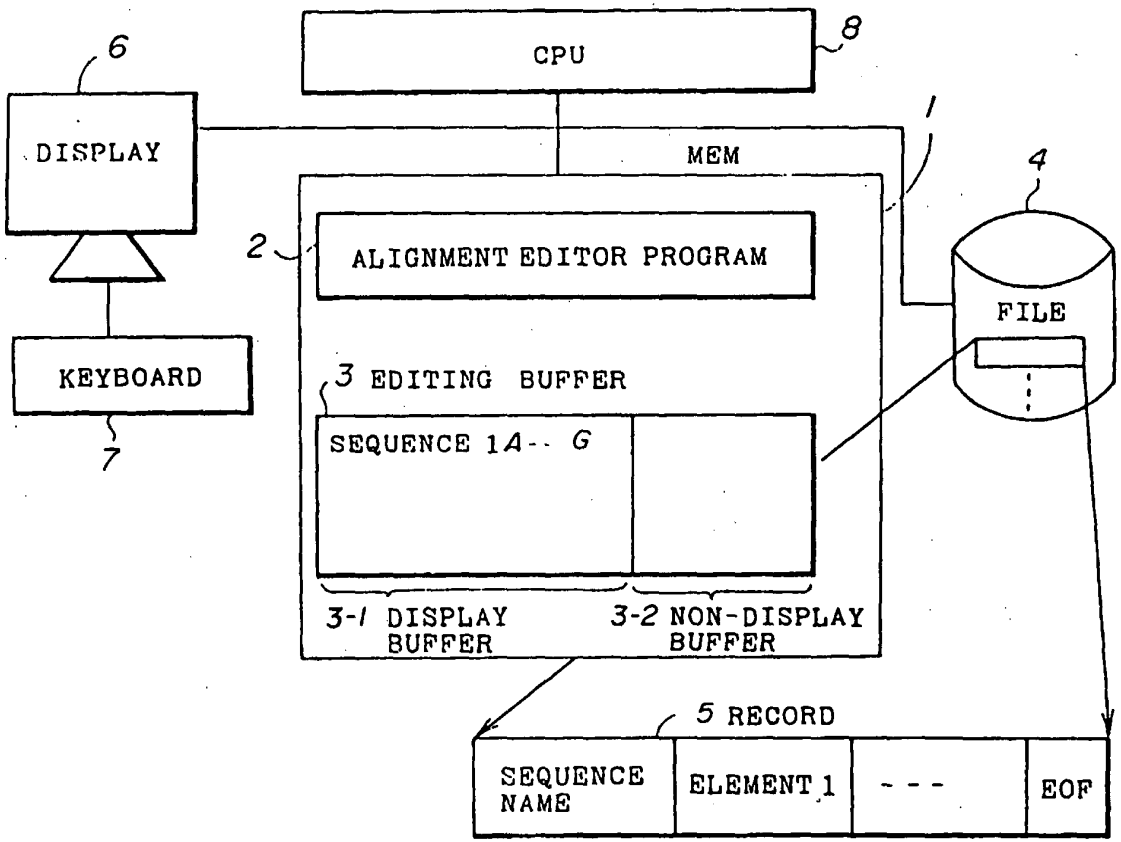
FIG.2


CPU
8
6
DISPLAY
1
MEM
4
2
ALIGNMENT EDITOR PROGRAM
FILE
KEYBOARD
3 EDITING BUFFER
7
SEQUENCE 1A-- G
3-1 DISPLAY BUFFER
3-2 NON-DISPLAY BUFFER
5 RECORD
SEQUENCE NAME
ELEMENT 1

EOF

BACKGROUND OF THE INVENTION

The present invention generally relates to parallel information display systems, and more particularly to a parallel information display system which enables analysis and editing of information relative to other information which is displayed in parallel therewith. The present invention is particularly suited for application to a genetic information analyzing and editing apparatus.

In biology and biology utilizing fields, there is a demand to realize an editing apparatus which enables simple analysis of a plurality of genetic sequences.

Conventionally, when displaying the genetic sequences on a display for analysis and editing the genetic sequences by inserting a gene depending on the analysis, the genetic sequences are displayed as shown in FIG.1. That is, elements S_{11}, S_{12}, ... of a genetic sequence having a sequence name "1" (for example, human) are displayed within a first block, and elements S_{21}, S_{22}, ... of another genetic sequence having a sequence name "2" (for example, ape) are displayed within a second block which is independent of the first block. When analyzing the genetic sequences, an element S_X within the first block is compared with an element S_Y within the second block, for example. An editing is made by inserting a desired element into the genetic sequence displayed within the first or second block so as to improve the degree of similarity of the two genetic sequences, for example.

However, the genetic sequence may have approximately 800 elements, and if the display is only capable of displaying 80 elements per line, the display of one genetic sequence may extend for ten lines. As a result, there is a problem in that it is difficult to compare one element within one of the ten lines of one block with one element within one of the ten lines of another block. The comparison becomes more difficult particularly when the elements to be compared are displayed at non-corresponding positions within the respective blocks. For example, the elements to be compared may be located at a second leftmost position in a fourth line of the first block and at a tenth leftmost position in a third line of the second block, and in this case, the operator must shift his eyes back and forth between the non-corresponding positions within the two blocks when making the analysis.

The editing of the genetic sequence is also difficult because the operator must shift his eyes back and forth between the two blocks in order to judge the similarity of the genetic sequences displayed in the two blocks. The analysis and editing becomes even more difficult when more than two genetic sequences are analyzed and edited simultaneously, since the first block and the last block may be quite separated from each other on the display and the simultaneous display of all of the desired blocks on the display may be impossible.

SUMMARY OF THE INVENTION

Accordingly, it is a general object of the present invention to provide a novel and useful parallel information display system in which the problems described above are eliminated.

Another and more specific object of the present invention is to provide a parallel information display system comprising display means, memory means for storing at least a sequence name and elements of a sequence for a plurality of sequences, input means for specifying a plurality of sequences to be displayed on the display means, and control means coupled to the display means, the memory means and the input means for controlling at least a read operation from the memory means responsive to the input means so that the sequence names and the elements of the specified sequences are displayed on the display means in units of blocks, where each of the blocks include the elements of the specified sequences displayed in adjacent lines in correspondence with the sequence names and each line is made up of a predetermined number of the elements of one of the specified sequences. According to the parallel information display system of the present invention, it is possible to display the elements of the sequences to be compared at adjacent lines of the same block, thereby making the comparison easy. Hence, the analysis and editing of the sequences can be made with ease within a relatively short time. The present invention is particularly effective when applied to a genetic information analyzing and editing apparatus because the number of elements forming each sequence is relatively large.

Other objects and further features of the present invention will be apparent from the following detailed description when read in conjunction with the accompanying drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG.1 is a diagram for explaining an example of a conventional display arrangement;

F1G.2 is a system block diagram showing a first embodiment of a parallel information display system according to the present invention;

FIG.3 is a flow chart for explaining a display process of the first embodiment;

FIG.4 is a flow chart for explaining an editing process of the first embodiment;

FIGS.5A through 5C are diagrams for explaining an operation of the first embodiment;

FIGS.6A through 6C are diagrams for explaining examples of genetic sequences;

FIG.7 is a system block diagram showing a second embodiment of the parallel information dis-

play system according to the present invention;
FIG.8 is a diagram for explaining an operation of the second embodiment; and
FIG.9 is a flow chart for explaining a display process of the second embodiment.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

FIG.1 shows a first embodiment of a parallel information display system according to the present invention. In this embodiment, the present invention is applied to a genetic information analyzing and editing apparatus. The parallel information display system includes a memory 1, a file 4, a display 6, a keyboard 7 and a central processing unit (CPU) 8 which are connected as shown.

The memory 1 includes an alignment editor program 2 and an editing buffer 3. The editing buffer 3 is made up of a display buffer 3-1 and a non-display buffer 3-2. The alignment editor program 2 carries out various editing processes such as storing genetic sequences in the editing buffer 3, while the display buffer 3-1 stores data to be displayed on the display 6. The non-display buffer 3-2 stores overflow data which overflow from the display buffer 3-1. The data stored in the display buffer 3-1 are sequence names of the genetic sequences, elements of the genetic information and the like. For example, the data overflow from the display buffer 3-1 when a character representing the genetic information is inserted at an arbitrary position within the display buffer 3-1. The editing buffer 3 edits and successively displays a plurality of genetic sequences on adjacent lines.

The file 4 stores the genetic information in the form of records 5. As shown in FIG.2, each record 5 includes elements "1", "2", ... and end of file (EOF) in correspondence with each sequence name.

The display 6 displays data such as the data stored in the display buffer 3-1 of the editing buffer 3. The keyboard 7 is used to move a cursor to an arbitrary position of the genetic sequences displayed on the display 6 and to input a character representing the genetic information at the cursor position.

As shown in FIG.2, the alignment editor program 2 successively stores the elements (genes) into the display buffer 3-1 of the editing buffer 3 in units of lines for a plurality of specified sequence names, and one line of elements from each sequence name forms a block. When all of the elements of the sequence name cannot be stored within the block, the remaining elements are stored within a next block and such an operation is repeated. The elements stored in the display buffer 3-1 of the editing buffer 3 are displayed on the display 6, and one or more elements may be inserted into a selected line by moving the cursor to an arbitrary position in the selected line. When the elements stored in the display buffer 3-1 for the selected line overflow from the display buffer 3-1 when this insertion is made, the elements which overflow from the display buffer 3-1 are stored in the non-display buffer 3-2. The elements stored in the non-display buffer 3-2 are stored in the display buffer 3-1 together with the elements of the next line if necessary.

Next, a description will be given of a display process of the first embodiment, by referring to FIG.3. In FIG.3, a step S11 specifies the file name. A step S12 specifies the sequence names. For example, the sequence names "Sequence 1", "Sequence 2" and "Sequence 3" are specified. The file and sequence names are specified from keys of the keyboard 7 by inputting the file and sequence names of a genetic sequence which is to be analyzed and edited.

A step S13 reads the specified genetic sequences. The specified genetic sequences are read by the alignment editor program 2 which reads from the file 4 the records 5 corresponding to the file and sequence names which are specified in the steps S11 and S12, and transfers the records 5 into the memory 1.

A step S14 displays one of the specified sequence names on the display 6. The sequence name is displayed by extracting the sequence name from the corresponding record 5 which is stored in the memory 1 and storing the sequence name from the start of the display buffer 3-1 of the editing buffer 1. For example, the sequence name "Sequence 1" shown in FIG.5A is displayed on the display 6.

A step S15 displays the genes which amount to to a predetermined length and correspond to the specified sequence name. For example, the genes which amount to one line (predetermined length) and correspond to the sequence name "Sequence 1" are stored in the display buffer 3-1 following the sequence name "Sequence 1". The genes "ATTAGCTG" are stored next to the sequence name "Sequence 1" as shown in FIG.5A.

A step S16 judges whether or not one line of genes is displayed for all of the specified sequence names, that is, whether or not the display of a block 1 shown in FIG.5A is ended. When the judgement result in the step S16 is NO, the process returns to the step S14 and the steps S14 and S15 are repeated. Hence, one line of genes is displayed for each of the sequence names "Sequence 1", "Sequence 2" and "Sequence 3" and the display of the block 1 is made by the repetition of the steps S14 and 15.

On the other hand, when the judgement result in the step S16 is YES, a step S17 judges whether or not one or more genes of the specified sequence names remain to be displayed. When the judgement result in the step S17 is YES, a step S18 starts the display for a next block 2 and the process returns to the step S14. As a result, the next block 2 is stored as shown in FIG.5A and displayed. The process ends when the judgement result in the step S17 becomes NO.

Therefore, the genes (elements) of the genetic

sequences having the sequence names specified by the operator are displayed in units of blocks, where each block is made up of one line of each of the specified sequence names. According to this display arrangement, it is easy for the operator to compare and analyze the genes of the specified sequence names on the display.

In FIG.5A and FIGS.5B, 5C, 6A through 6C and 8 which follow, "A" denotes adenine, "G" denotes guanine, "T" denotes thymine and "C" denotes cytosine. In addition, FIGS.5A through 5C respectively show the arrangement of data within the display buffer 3-1 and the non-display buffer 3-2 of the editing buffer 3 in correspondence with the display 6. Hence, the data stored in the display buffer 3-1 are displayed on the display 6 as indicated by "Display Range" in FIG.5C, while the data stored in the non-display buffer 3-2 are not displayed on the display 6. Therefore, the arrangement of the data within the display buffer 3-1 is essentially the same as the display arrangement on the display 6.

Next, a description will be given of an editing process of the first embodiment during an editing mode, by referring to FIG.4. In FIG.4, a step S21 moves the cursor to an arbitrary position where a character or gap is to be inserted by manipulating the keyboard 7. A step S22 inputs the character which is to be inserted from the key of the keyboard 7. For example, the gap may be inserted by inputting a predetermined character or symbol from the keyboard 7.

A step S23 moves the characters which are positioned at and after the inserting position and displays the characters at new moved positions. When one character is inserted, the characters positioned at and after the inserting position are displayed at positions which are respectively shifted by one character from the respective original display positions.

For example, the step S21 moves the cursor to the position of the character "T" in FIG.5A, and the step S22 inputs a character "*" from the keyboard 7 as shown in FIG.5B, As a result, the step S23 moves the characters which are positioned at and after the inserting position by one character and displays the characters at the new moved positions as shown in FIG.5B. In other words, the characters "TAGCTG" positioned at and after the inserting position are displayed at positions shifted by one character to the right from the respective original display positions and the character "*" is displayed at the inserting position.

Thereafter, a step S24 judges whether or not an action key of the keyboard 7 is pushed. This action key specifies a revised display mode in which the edited result is displayed on the display 6. When the judgement result in the step S24 is NO, the process returns to the step S21. On the other hand, when the judgement result in the step S24 is YES, the process advances to a step S25.

The step S25 reads the data amounting to one line from the editing buffer 3. In other words, the sequence name and the corresponding genes in one line are read out from the display buffer 3-1 and the non-display buffer 3-2. A step S26 extracts only the genes which are read in the step S25 and connects the genes. A step S27 judges whether or not all of the genes of the sequence name are read one line at a time and connected for all lines. When the judgement result in the step S27 is NO, the process returns to the step S25 to read the data amounting to another line from the editing buffer 3. The steps S25 and S26 are repeated until the judgement result in the step S27 becomes YES.

When the judgement result in the step S27 is YES, a step S28 displays the genes in units of lines again, so that all of the genes temporarily stored in the non-display buffer 3-2 are now stored in the display buffer 3-1 and displayed on the display 6. The step S28 is carried out by advancing to the step S14 shown in FIG.3. As a result, the data arrangement within the editing buffer 3 and thus the display on the display 6 changes from that shown in FIG.5B to that shown in FIG.5C.

Therefore, by the above described process, the character is inserted in units of lines by moving the cursor to an arbitrary character position of a block and inputting the character from the keyboard 7. The process of displaying the elements of all of the genetic sequences in units of blocks may be carried out again if necessary. Hence, the elements of the genetic sequences to be compared are displayed at adjacent lines so that the analysis (comparison) and the necessary insertion can be made promptly.

As described above, FIGS.5A through 5C show the data stored in the display buffer 3-1 and the non-display buffer 3-2 of the editing buffer 3. Only the data stored in the display buffer 3-1, such as the sequence name and the genes, are displayed on the display 6.

FIG.5A shows an initial state where the genetic sequences "1", "2" and "3" are specified and the data are stored in the display buffer 3-1 by the processes of the steps S11 through S17 shown in FIG.3.

FIG.5B shows a state where one character "*" is inserted in the genetic sequence "1" and the two characters "*" are inserted in the genetic sequence "3". In this case, the rightmost character "G" of the first line of the genetic sequence "1" overflows from the display buffer 3-1 and is stored in the non-display buffer 3-2. Similarly, two rightmost characters "C" and "A" of the first line of the genetic sequence "3" overflow from the display buffer 3-1 and are stored in the non-display buffer 3-2. The characters (data) stored in the non-display buffer 3-2 are not displayed on the display 6.

FIG.5C shows a state after the display process is carried out again in the state shown in FIG.5B. This display is carried out by the processes of the steps S25 through S28 shown in FIG.4 when the action key

of the keyboard 7 is pushed in the step S24.

FIG.6A shows DNA sequences as examples of the genetic sequences. The gene in this case is made up of four kinds of bases which are adenine (A), guanine (G), thymine (T) and cytosine (C). When the DNA sequences are displayed in units of blocks as in the first embodiment, the first block displays four sequence names "KRI1", "KRI2", "KRI24" and "KRI30" as shown in FIG.6A, for example.

FIG.6B shows protein sequences as examples of the genetic sequences. Protein is formed when three bases are grouped, and the protein is determined by the combination of the bases. In FIG.6B, "H" denotes histidine, "N" denotes asparagine and "S" denotes serine.

FIG.6C shows a genetic code table which shows the relationship of the grouped bases and the formed protein. In FIG.6C, the following abbreviations are used.

Ala : Alanine
Arg : Arginine
Asn : Asparagine
Asp : Aspartic Acid
Cys : Cysteine
Gln : Glutamine
Glu : Glutamic Acid
Gly : Glycine
His : Histidine
Ile : Isoleucine
Leu : Leucine
Lys : Lysine
Met : Methionine
Phe : Phenylalanine
Pro : Proline
Ser : Serine
Thr : Threonine
Trp : Tryptophan
Tyr : Tyrosine
Val : Valine

In this embodiment, the inserting operation is described as an example of the editing operation. However, copy, move and delete operations can be carried out similarly as in the case of the inserting operation. In other words, the data which overflows from the display buffer 3-1 is stored in the non-display buffer 3-2. On the other hand, when the number of characters of one line within the block becomes smaller than the maximum number of characters displayed in one line, a unique data such as "0" is stored in the display buffer 3-1 as shown in FIG.6B. When the unique data such as "0" is stored in the display buffer 3-1, only the significant data stored in the display buffer 3-1 are displayed on the display 6 and the unique data "0" is not displayed.

The first embodiment was tested by operating the parallel information display system on the UNIX system. An editing operation was carried out for four Kringle DNA sequences respectively having a length of 234 characters, and genes or gaps amounting to fifteen characters were inserted in a line. It was confirmed that the analysis and the editing operation are facilitated by the display of the sequences in units of blocks each having a line of the sequences to be analyzed.

Next, a description will be given of a second embodiment of the parallel information display system according to the present invention. FIG.7 shows the second embodiment. In FIG.7, those parts which are the same as those corresponding parts in FIG.2 are designated by the same reference numerals, and a description thereof will be omitted.

In this second embodiment, the memory 1 shown in FIG.7 includes a scale data 100 for displaying a fixed scale in correspondence with each block so as to facilitate the location of each element of each line within the block. FIG.8 shows an example of the display which is made on the display 6 when the same data shown in FIG.5A are displayed. In FIG.8, the scale indicates the element numbers "1" to "8" in the first block, and indicates the element numbers "9" to "16" in the second block. Although not shown, it is also possible to display the block numbers together with the scale.

FIG.9 shows a flow chart for explaining the display process of the second embodiment. In FIG.9, those steps which are the same as those corresponding steps in FIG.3 are designated by the same reference numerals, and a description thereof will be omitted. In FIG.9, a step S101 initializes the count to zero. A step S102 increments the count by one, and a step S103 reads the scale data 100 corresponding to the count from the memory 1. The number of characters displayed in one line is known, and is eight in this case. Hence, when the count is "1", the corresponding scale data 100 includes the necessary information to display the scale numbers "1" to "8" as shown in FIG.8. A step S14A displays the scale data 100 read from the memory 1 together with the sequence names in the first block, and the process advances to the step S15. The scale for the second and subsequent blocks are similarly displayed when the sequence names in the subsequence blocks are displayed.

According to this second embodiment, the provision of the scale makes it even easier to locate the elements of the genetic sequences, thereby facilitating the analysis and editing of the genetic sequences.

In the described embodiments, the present invention is applied to the genetic information analyzing and editing apparatus. However, the present invention may be applied to apparatuses other than the genetic information analyzing and editing apparatus as long as information sequences need to be compared. For example, in a speech recognition apparatus, a standard speech information sequence which is registered in advance is compared with an

input speech information sequence in order to recognize the input speech information sequence, and the present invention is also applicable to such a speech recognition apparatus.

Claims

1. A parallel information display system comprising display means (6), memory means (4) for storing at least a sequence name and elements of a sequence for a plurality of sequences, and input means (7) for specifying a plurality of sequences to be displayed on said display means, characterized in that there is provided: control means (8), coupled to said display means (6), said memory means (4) and said input means (7), for controlling at least a read operation from said memory means (4) responsive to said input means so that the sequence names and the elements of the specified sequences are displayed on said display means in units of blocks, each of said blocks including the elements of the specified sequences displayed in adjacent lines in correspondence with the sequence names, each line being made up of a predetermined number of the elements of one of the specified sequences.

2. The parallel information display system as claimed in claim 1, characterized in that there is further provided a memory (1) for storing fixed scale information, and said control means (8) reads the fixed scale information from said memory together with the sequence names and the elements of the specified sequences from said memory means to display on said display means (6) a fixed scale together with each block to indicate positions of each element in the line.

3. The parallel information display system as claimed in claim 1 or 2, characterized in that said input means (7) includes keys which are manipulated during an editing mode in which the elements of an arbitrary block which is displayed on said display means (6) are edited, said editing mode including insertion, deletion, copying and moving of the element.

4. The parallel information display system as claimed in claim 3, characterized in that there are further provided first and second buffer means (3-1, 3-2) for temporarily storing the sequence names and the elements of the specified sequences which are read out from said memory means (4) under a control of said control means (8), said first buffer means (3-1) storing the sequence names and the elements which are to be displayed on said display means (6) in units of blocks, said second buffer means (3-2) storing the elements which overflow from said first buffer means during the editing mode and are not to be displayed on said display means, said control means reading the sequence names and the elements from said first buffer means and displaying the same on said display means.

5. The parallel information display system as claimed in claim 4, characterized in that said control means (8) automatically stores one or more elements of a line which exceed the predetermined number during the editing mode into said second buffer means (3-2) for each line within the arbitrary block.

6. The parallel information display system as claimed in claim 5, characterized in that said input means (7) includes an action key which is manipulated during a revised display mode in which an edited result is displayed on said display means (6), said control means (8) automatically storing the elements stored in said first and second buffer means (3-1, 3-2) into said first buffer means (3-1) in units of blocks when said action key is manipulated.

7. The parallel information display system as claimed in any of claims 1 to 6, characterized in that said control means (8) displays the elements of each block in groups of a predetermined number of elements.

8. The parallel information display system as claimed in any of claims 1 to 7, characterized in that the elements of each sequence are genes of a genetic sequence.

9. The parallel information display system as claimed in any of claims 1 to 7, characterized in that the sequences are selected from a group consisting of sequences of genetic information and speech information.

FIG. 1 PRIOR ART

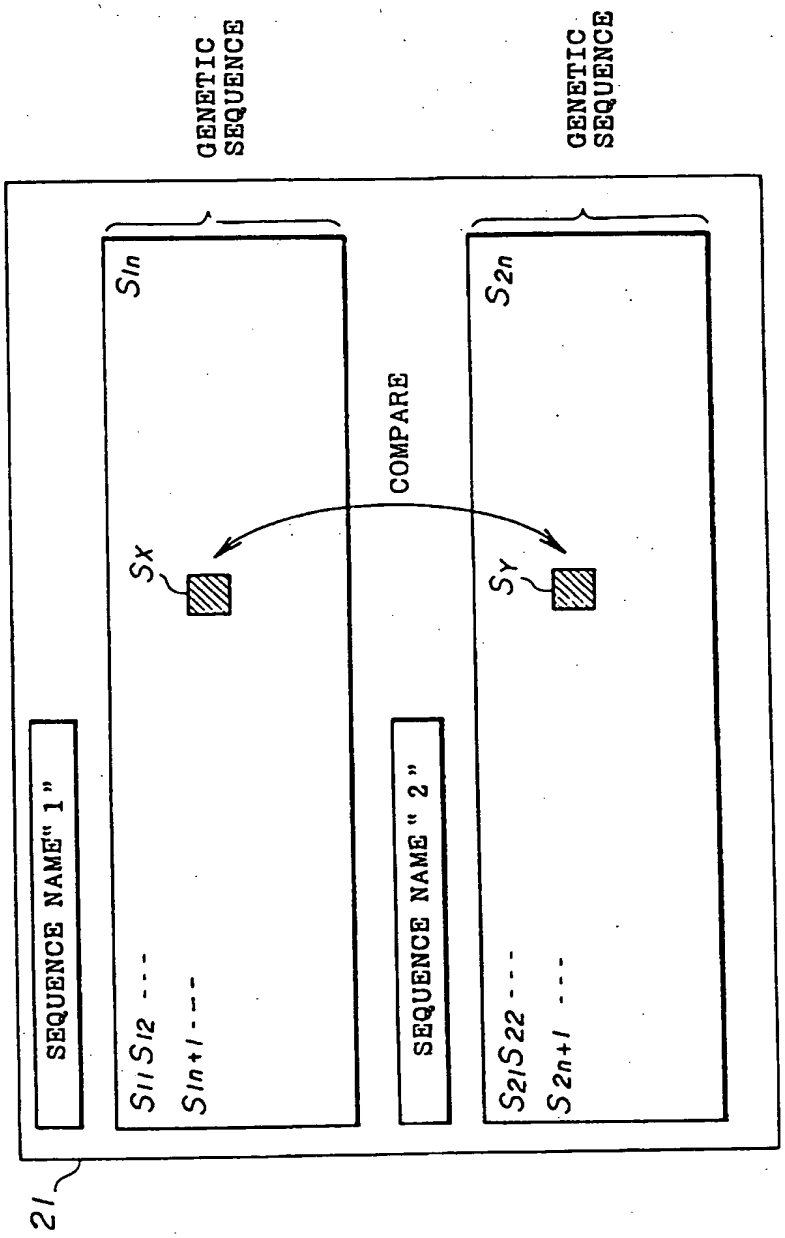


FIG.2

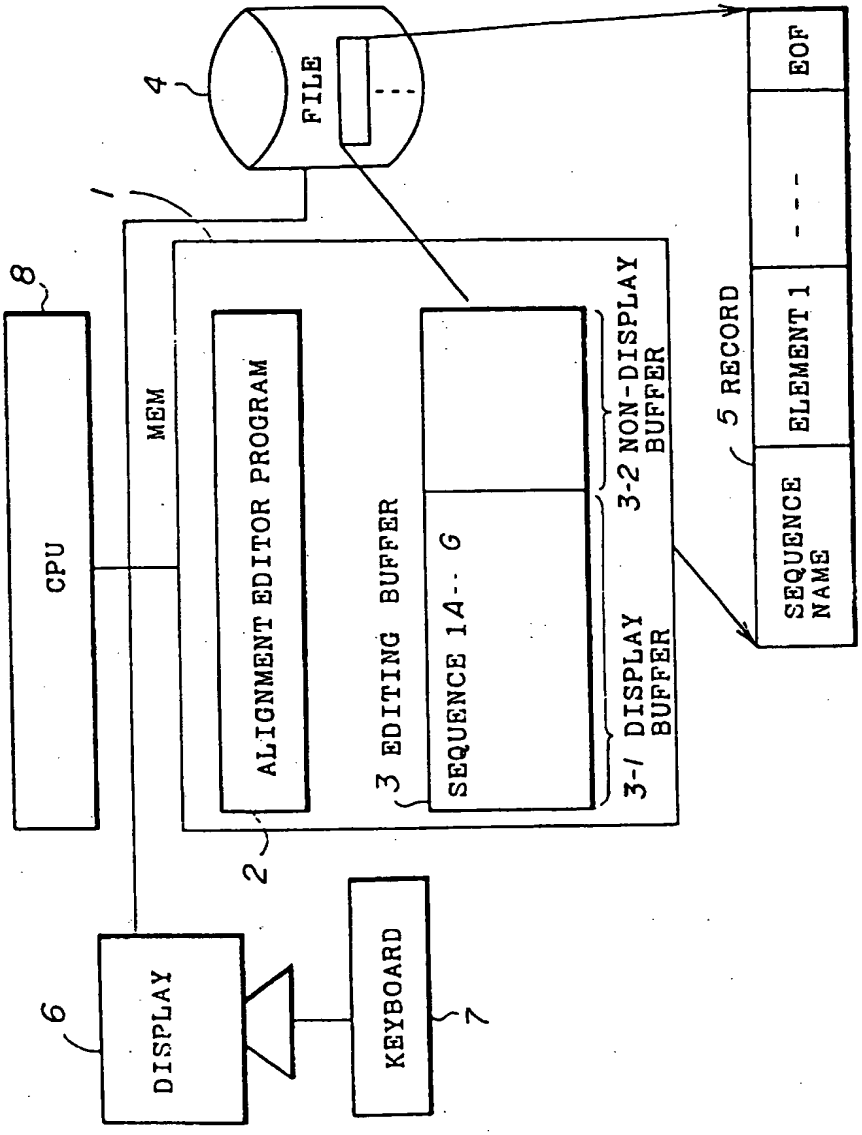

4
FILE
1
8
CPU
MEM
ALIGNMENT EDITOR PROGRAM
3 EDITING BUFFER
SEQUENCE 1A-- G
3-2 NON-DISPLAY BUFFER
3-1 DISPLAY BUFFER
2
5 RECORD
SEQUENCE NAME
ELEMENT 1
- - -
EOF
6
DISPLAY
KEYBOARD
7

FIG.3

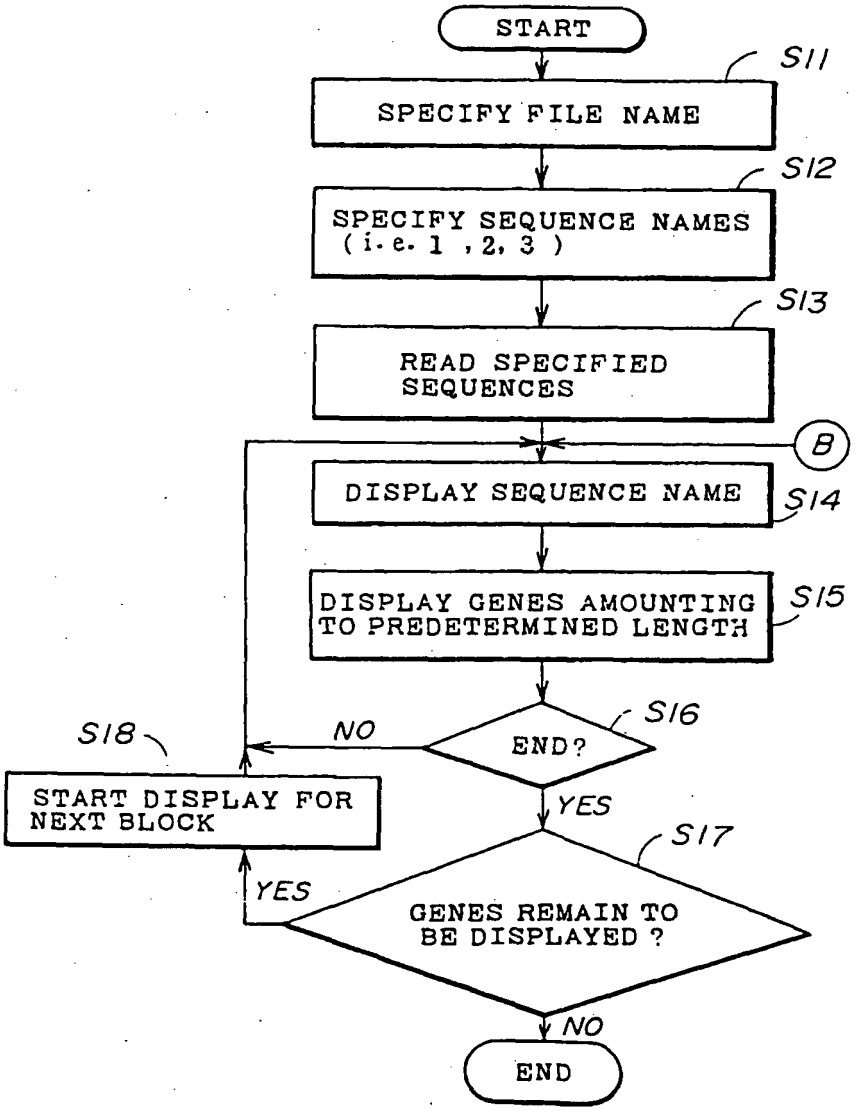

START
S11
SPECIFY FILE NAME
S12
SPECIFY SEQUENCE NAMES
(i.e. 1 , 2, 3)
S13
READ SPECIFIED SEQUENCES
B
DISPLAY SEQUENCE NAME
S14
DISPLAY GENES AMOUNTING TO PREDETERMINED LENGTH
S15
S16
END?
NO
S18
START DISPLAY FOR NEXT BLOCK
YES
S17
YES
GENES REMAIN TO BE DISPLAYED ?
NO
END

FIG. 4

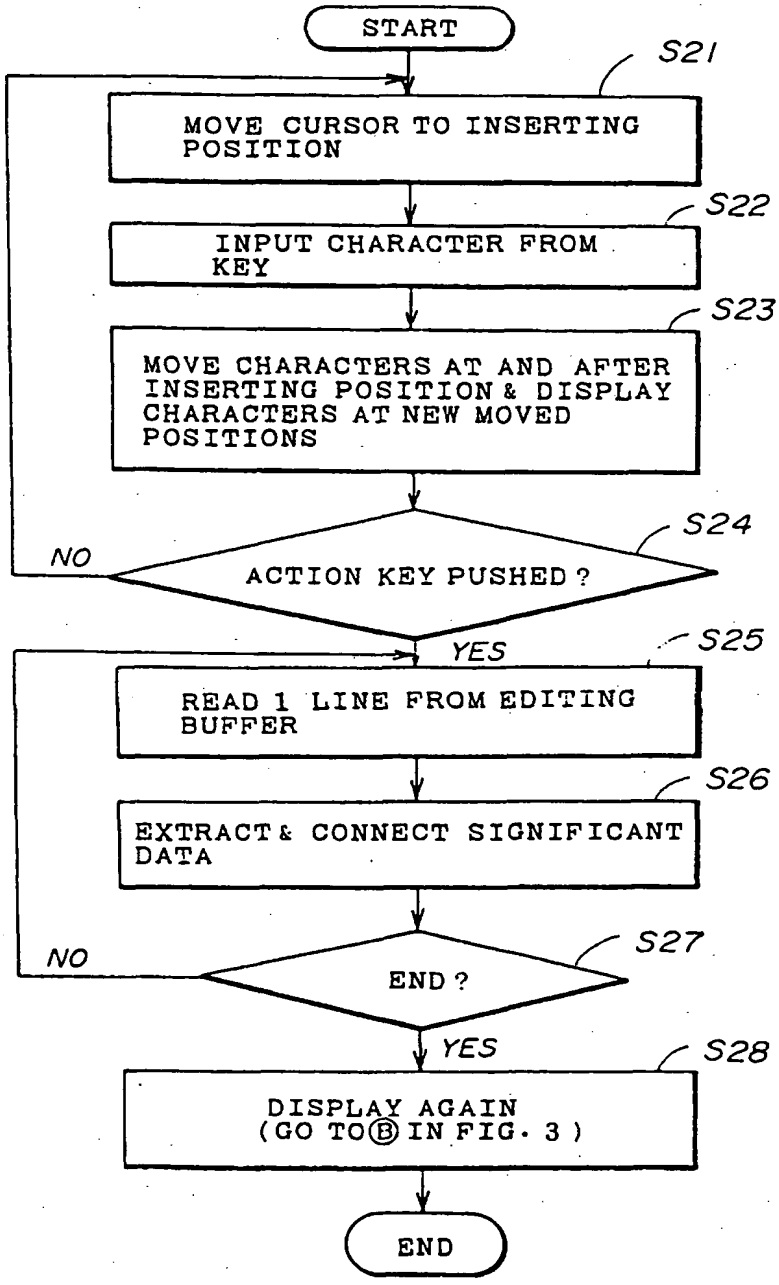

START
S21
MOVE CURSOR TO INSERTING POSITION
S22
INPUT CHARACTER FROM KEY
S23
MOVE CHARACTERS AT AND AFTER INSERTING POSITION & DISPLAY CHARACTERS AT NEW MOVED POSITIONS
S24
ACTION KEY PUSHED ?
NO
YES
S25
READ 1 LINE FROM EDITING BUFFER
S26
EXTRACT & CONNECT SIGNIFICANT DATA
S27
END ?
NO
YES
S28
DISPLAY AGAIN (GO TO Ⓑ IN FIG. 3)
END

FIG.5A

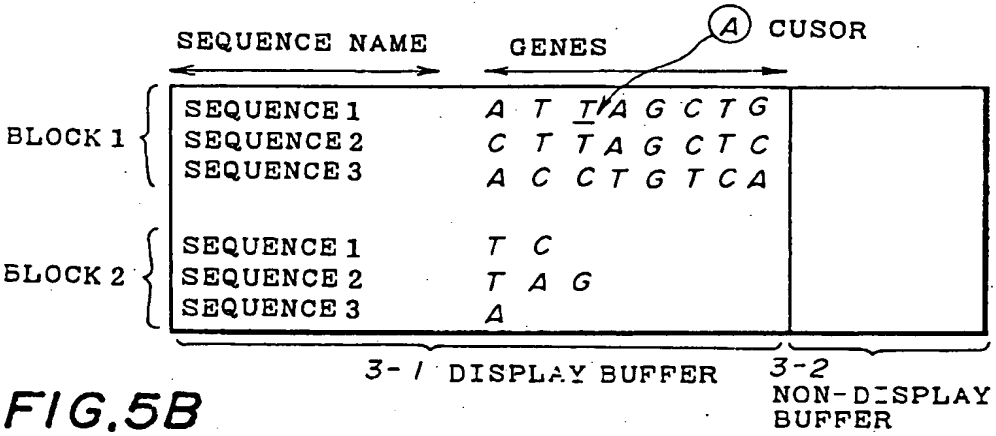


FIG.5B

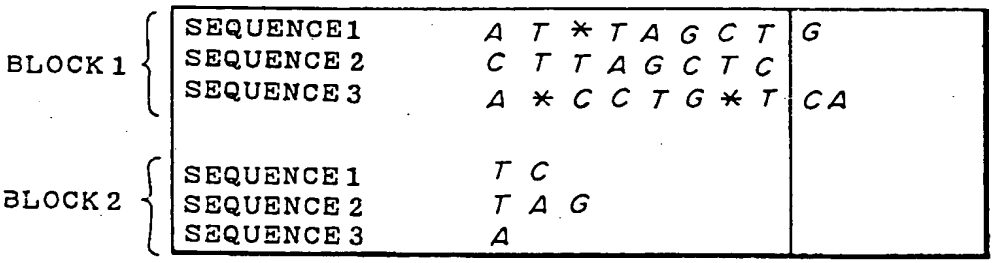


FIG.5C

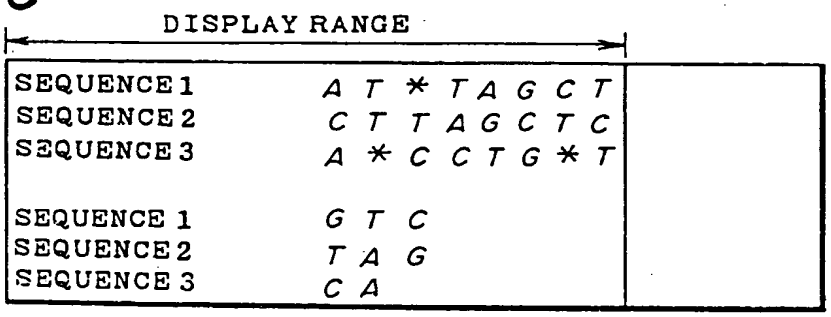


FIG.6A

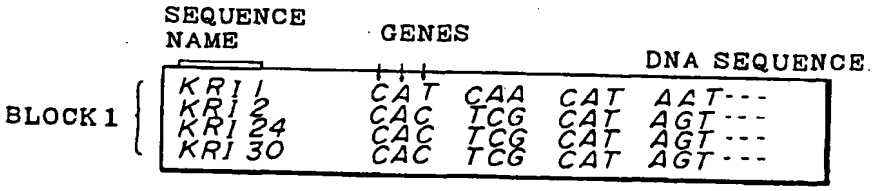


FIG.6B

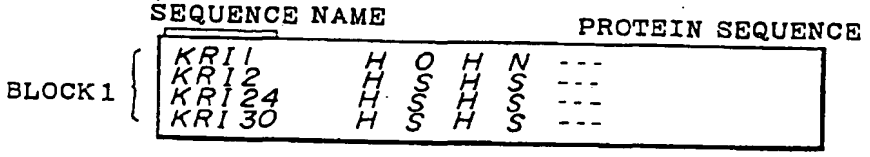


FIG.6C

GENETIC CODE TABLE

1ST CHARACTER	2ND CHARACTER: U	C	A	G	3RD CHARACTER
U	UUU, UUC } Phe	UCU, UCC, UCA, UCG } Ser	UAU, UAC } Tyr	UGU, UGC } Cys	U
	UUA, UUG } Leu		UAA, UAG } END	UGA } END UGG } Trp	C A G
C	CUU, CUC, CUA, CUG } Leu	CCU, CCC, CCA, CCG } Pro	CAU, CAC } His CAA, CAG } Gln	CGU, CGC, CGA, CGG } Arg	U C A G
A	AUU, AUC, AUA } Ile AUG } START	ACU, ACC, ACA, ACG } Thr	AAU, AAC } Asn AAA, AAG } Lys	AGU, AGC } Ser AGA, AGG } Arg	U C A G
G	GUU, GUC, GUA, GUG } Val	GCU, GCC, GCA, GCG } Ala	GAU, GAC } Asp GAA, GAG } Glu	GGU, GGC, GGA, GGG } Gly	U C A G

FIG. 7

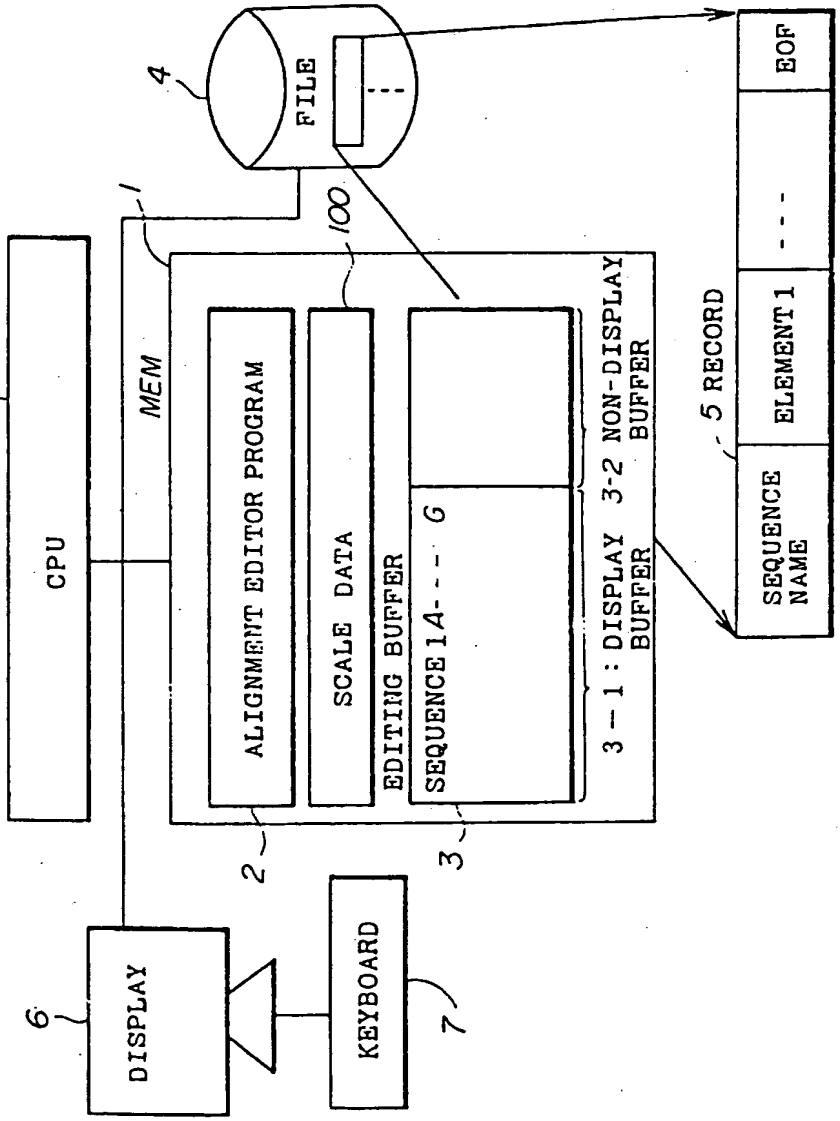

4
FILE
EOF
1
100
8
CPU
MEM
ALIGNMENT EDITOR PROGRAM
SCALE DATA
EDITING BUFFER
SEQUENCE 1A- - - G
3-1 : DISPLAY BUFFER
3-2 NON-DISPLAY BUFFER
5 RECORD
SEQUENCE NAME
ELEMENT 1
- - -
2
3
6
DISPLAY
KEYBOARD
7

FIG.8

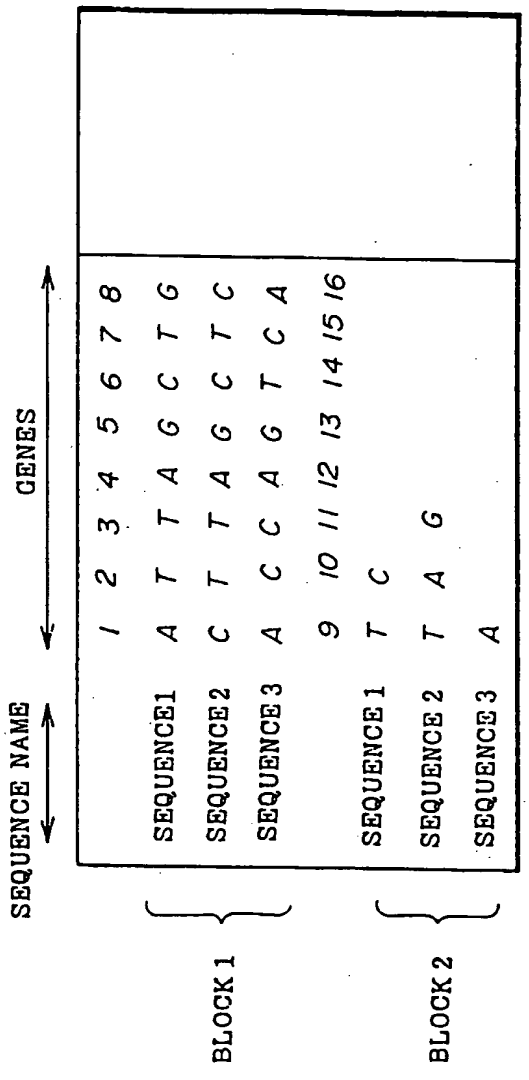
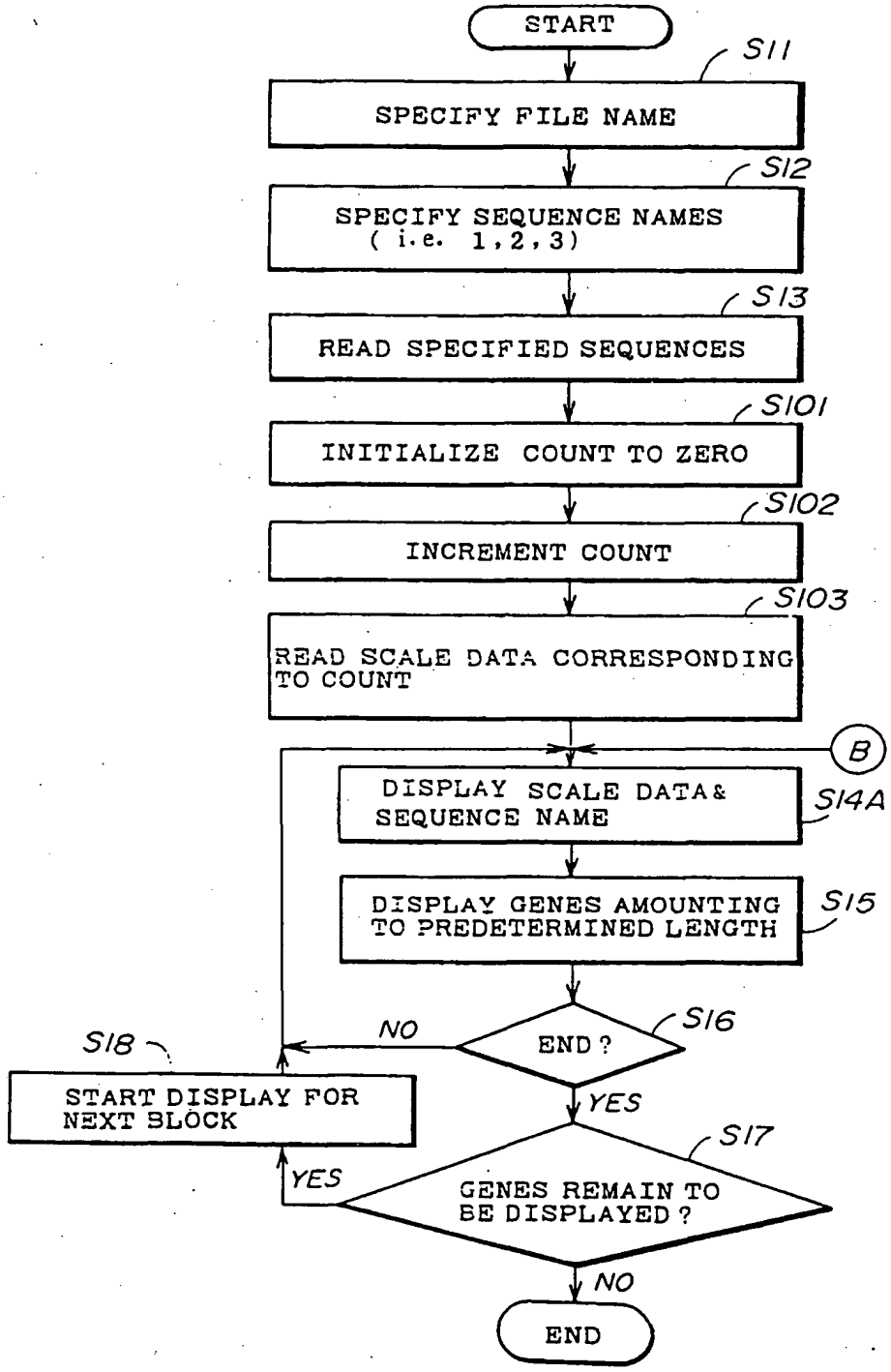

SEQUENCE NAME
GENES
1 2 3 4 5 6 7 8
SEQUENCE1 A T T A G C T G
SEQUENCE 2 C T T A G C T C
SEQUENCE 3 A C C A G T C A
9 10 11 12 13 14 15 16
SEQUENCE 1 T C
SEQUENCE 2 T A G
SEQUENCE 3 A
BLOCK 1
BLOCK 2

FIG. 9


START
S11
SPECIFY FILE NAME
S12
SPECIFY SEQUENCE NAMES
(i.e. 1,2,3)
S13
READ SPECIFIED SEQUENCES
S101
INITIALIZE COUNT TO ZERO
S102
INCREMENT COUNT
S103
READ SCALE DATA CORRESPONDING TO COUNT
B
DISPLAY SCALE DATA& SEQUENCE NAME
S14A
DISPLAY GENES AMOUNTING TO PREDETERMINED LENGTH
S15
END ?
S16
NO
S18
START DISPLAY FOR NEXT BLOCK
YES
S17
GENES REMAIN TO BE DISPLAYED ?
YES
NO
END